In the Claims:

Claim 1 (Currently amended): An isolated polynucleotide comprising a nucleotide sequence encoding a polypeptide having at least 9580% sequence identity with SEQ ID NO: ~~20~~ 21 as determined using a sequence analysis software package developed by the Genetic Computer Group (GCG) at the University of Wisconsin with gap creation penalty of 50 and gap extension penalty of 3, ~~and/or hybridizable with SEQ ID NO:20 under conditions of stringent hybridization, wherein said stringent hybridization is effected by a hybridization solution of 6 x SSC and 1 % SDS, hybridization temperature of 65 °C, final wash solution of 0.1 x SSC and final wash at 60 °C,~~ saidthe ~~isolated polynucleotide encoding a~~ polypeptide having a flavanone-7-*O*-glucoside-2"-*O*-rhamnosyl-transferase catalytic activity.

Claim 2 (Original): The isolated polynucleotide of claim 1, wherein said nucleotide sequence is selected from the group consisting of DNA and RNA.

Claim 3 (Original): The isolated polynucleotide of claim 1, wherein said nucleotide sequence is selected from the group consisting of complementary DNA, genomic DNA and messenger RNA.

Claim 4 (Original): The isolated polynucleotide of claim 1, further comprising a vector, wherein said nucleotide sequence is ligated to said vector.

Claim 5 (Previously presented): The isolated polynucleotide of claim 4, wherein said vector is an expression vector, and whereas said nucleotide sequence is operably linked to a promoter sequence.

Claim 6 (Original): The isolated polynucleotide of claim 5, wherein said nucleotide sequence is ligated to said vector in an orientation selected from the group consisting of a sense orientation and an antisense orientation.

Claim 7 (Original): The isolated polynucleotide of claim 5, wherein said vector is selected from the group consisting of a vector propagatable in plant cells and a vector propagatable in a microorganism cell.

Claim 8 (Previously presented): The isolated polynucleotide of claim 5, wherein said nucleotide sequence is as set forth in SEQ ID NO:20.

Claims 9-10 (Canceled).

Claim 11 (Previously presented): The isolated polynucleotide of claim 1, wherein said polypeptide is as set forth in SEQ ID NO:21.

Claim 12 (Currently amended): The isolated polynucleotide of claim 1 as set forth in SEQ ID NO:20, ~~wherein said polypeptide shares at least 75 % identical or conserved amino acids with SEQ ID NO:21, as determined using a sequence analysis software package developed by the Genetic Computer Group (GCG) at the University of Wisconsin with gap creation penalty of 12 and gap extension penalty of 4~~.

Claim 13 (Original): The isolated polynucleotide of claim 1, wherein said nucleotide sequence originates from a species of the genus *Citrus*.

Claim 14- 23 (Canceled)

Claim 24 (Currently amended): A transgenic plant of a species naturally expressing a flavanone-7-*O*-glucoside-2"-*O*-rhamnosyl-transferase messenger RNA, wherein the transgenic plant is genetically modified to include an expressible polynucleotide comprising a nucleic acid sequence having at least 9580% sequence identity with SEQ ID NO: 20 as determined using a sequence analysis software package developed by the Genetic Computer Group (GCG) at the University of Wisconsin with gap creation penalty of 50 and gap extension penalty of 3, ~~and/or hybridizable with SEQ ID NO:20 under conditions of stringent hybridization, wherein said stringent hybridization is effected by a hybridization solution of 6 x SSC and 1 % SDS, hybridization temperature of 65 °C, final wash solution of 0.1 x SSC and final wash at 60 °C,~~ said polynucleotide designed encoding nucleotide sequences complementary to, and capable of binding to flavanone-7-O-glucoside-2"-O-rhamnosyl-transferase transcripts, and whereas expression of said expressible polynucleotide decreases the level of

flavanone-7-O-glucoside-2"-O-rhamnosyl-transferase catalytic activity in said plant cell.~~, in an expressible antisense orientation, a nucleotide sequence encoding an antisense RNA molecule being capable of *in vivo* base pairing with said flavanone-7-*O*-glucoside-2"-*O*-rhamnosyl-transferase messenger RNA, to thereby render said flavanone-7-*O*-glucoside-2"-*O*-rhamnosyl-transferase messenger RNA, when expressed, amenable to degradation by nucleases present in the transgenic plant.~~

Claim 25 (Original): The transgenic plant of claim 24, wherein said nucleotide sequence is selected from the group consisting of a complementary DNA and a genomic DNA.

Claim 26 (Original): The transgenic plant of claim 24, wherein said nucleotide sequence is extrachromosomal.

Claim 27 (Original): The transgenic plant of claim 24, wherein said nucleotide sequence is intrachromosomal.

Claim 28 (Original): The transgenic plant of claim 24, wherein said nucleotide sequence is ligated to an expression vector in antisense orientation.

Claim 29 (Previously presented): The transgenic plant of claim 28, wherein said nucleotide sequence is as set forth in SEQ ID NO:20

Claims 30- 33 (Canceled)

Claim 34 (Currently amended): A cell genetically modified to include, in an expressible sense orientation, a nucleotide sequence having at least 95~~80~~% sequence identity with SEQ ID NO: 20 as determined using a sequence analysis software package developed by the Genetic Computer Group (GCG) at the University of Wisconsin with gap creation penalty of 50 and gap extension penalty of 3,~~and/or hybridizable with SEQ ID NO:20 under conditions of stringent hybridization, wherein said stringent hybridization is effected by a hybridization solution of 6 x SSC and 1 % SDS, hybridization temperature of 65 °C, final wash solution of 0.1 x SSC and final~~

~~wash at 60 - the nucleotide sequence encoding a~~ said polypeptide having a flavanone-7-*O*-glucoside-2"-*O*-rhamnosyl-transferase activity.

Claim 35 (Original): The cell of claim 34, wherein said nucleotide sequence is selected from the group consisting of complementary DNA and genomic DNA.

Claim 36 (Original): The cell of claim 34, wherein said nucleotide sequence is extrachromosomal.

Claim 37 (Original): The cell of claim 34, wherein said nucleotide sequence is intrachromosomal.

Claim 38 (Original): The cell of claim 34, wherein said nucleotide sequence is ligated to an expression vector in sense orientation.

Claim 39 (Previously amended): The cell of claim 38, wherein said nucleotide sequence is as set forth in SEQ ID NO:20.

Claims 40-41 (Canceled).

Claim 42 (Original): The cell of claim 34, wherein said nucleotide sequence originates from a species of the genus *Citrus*.

Claim 43 (Original): The cell of claim 34, wherein the cell is of a microorganism.

Claim 44 (Original): The cell of claim 43, wherein said microorganism is producing activated rhamnose.

Claim 45 (Original): The cell of claim 43, wherein said microorganism is selected from the group consisting of *Lactobacillus* and *Saccharomyces*.

Claim 46 (Original): The cell of claim 34, wherein the cell is of a plant species.

Claim 47 (Original): The cell of claim 46, wherein said plant species is of a genus selected from the group consisting of *Citrus, Nicotiana, Vitis* and *Daucus*.

Claims 48-61 (Withdrawn).

Claims 62-83 (Cancelled).

Claim 84 (Currently amended): A method of modifying a level of a flavanone-7-*O*-glucoside-2"-*O*-rhamnosyl-transferase activity in a plant cell, the method comprising regulating the level of activity or expression of a 7-*O*-glucoside-2"-*O*-rhamnosyl-transferase mRNA~~gene~~ in the plant cell, said 7-*O*-glucoside-2"-*O*-rhamnosyl-transferase mRNA comprising a polynucleotide sequence being at least 95% complementary to SEQ ID NO: 20 as determined using a sequence analysis software package developed by the Genetic Computer Group (GCG) at the University of Wisconsin with gap creation penalty of 50 and gap extension penalty of 4, thereby modifying the level of a 7-*O*-glucoside-2"-*O*-rhamnosyl-transferase activity in the plant cell.

Claim 85 (Currently amended): The method of claim 84, wherein said regulation is upregulation and is effected by expressing within the plant cell an exogenous polynucleotide encoding a polypeptide having at least 95% sequence identity with SEQ ID NO: 21 as determined using a sequence analysis software package developed by the Genetic Computer Group (GCG) at the University of Wisconsin with gap creation penalty of 12 and gap extension penalty of 4, said polypeptide having 7-*O*-glucoside-2"-*O*-rhamnosyl-transferase activity.

Claim 86.(Currently amended): The method of claim 8~~4~~5, wherein said exogenous polynucleotide comprises a nucleic acid sequence as set forth in ~~having at least 80% nucleic acid sequence identity with~~ SEQ ID NO: 20.

Claim 87 (Canceled)

Claim 88 (Currently amended): A method of producing plant cells having a modified level of flavanone-7-*O*-glucoside-2"-*O*-rhamnosyl-transferase, the method effected by:

(a) providing an expressible polynucleotide comprising a nucleic acid sequence having at least 95~~80~~% nucleic acid sequence identity with SEQ ID NO: 20 operably linked to a plant-operable promoter sequence;

(b) transforming a population of plant cells with said expressible polynucleotide; and

(c) selecting a transformed plant cell having a modified level of a flavanone-7-*O*-glucoside-2"-*O*-rhamnosyl-transferase activity; and

(d) propagating said transformed plant cell having a modified level of a flavanone-7-*O*-glucoside-2"-*O*-rhamnosyl-transferase activity;

thereby producing plant cells having a modified level of flavanone-7-*O*-glucoside-2"-*O*-rhamnosyl-transferase.

Claim 89 (Previously presented): The method of claim 88, wherein said selecting is effected by determining in the plant cells at least one parameter selected from the group consisting of taste test of bitterness, flavanone-7-*O*-glucoside-2"-*O*-rhamnosyl-transferase catalytic activity, and flavanone-7-*O*-glucoside-2"-*O*-rhamnosyl-transferase antigenic activity.

Claim 90 (Currently amended): The method of claim 88, wherein said nucleic acid sequence having at least 95~~80~~% nucleic acid sequence identity with SEQ ID NO: 20 is oriented in a sense orientation, and whereas said transformed plant cells have an increased level of flavanone-7-*O*-glucoside-2"-*O*-rhamnosyl-transferase activity.

Claim 91 (Canceled)